

Systematic Gene Search in the Incyte LifeSeq Database

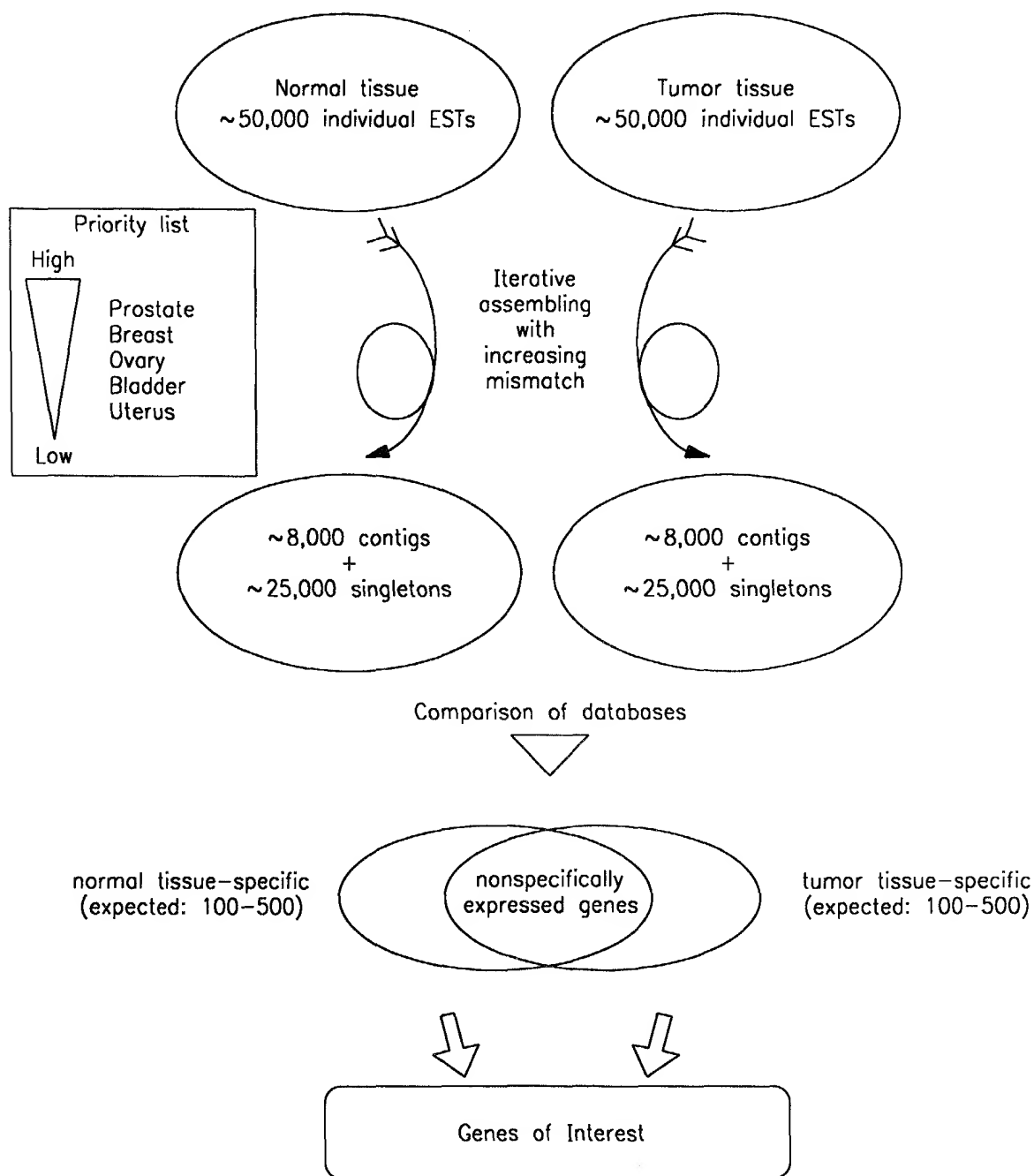
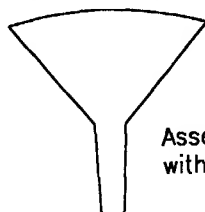


FIG. 1

APPROVED	O. G. FIG.
BY	CLASS SUBCLASS
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Principle of EST Assembly

~50,000 ESTs per tissue

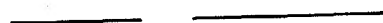
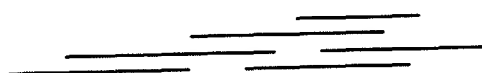


Assembly at 0% mismatch
with GAP4 (Staden)

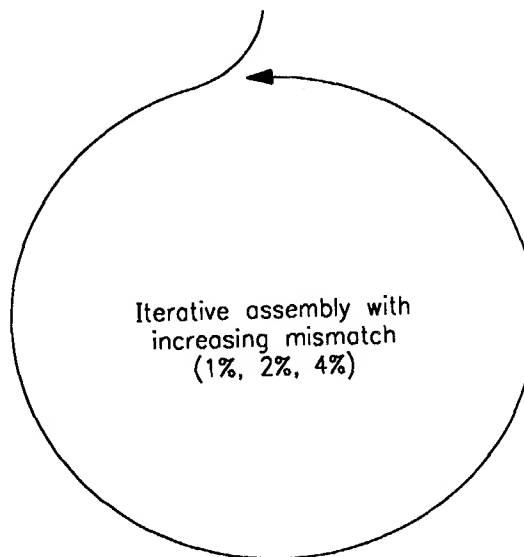


Contigs

Singletons



Contigs increasing in
number and length



Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 Contigs

~25,000 other singletons



~30,000 consensus-
sequences per tissue

FIG. 2a

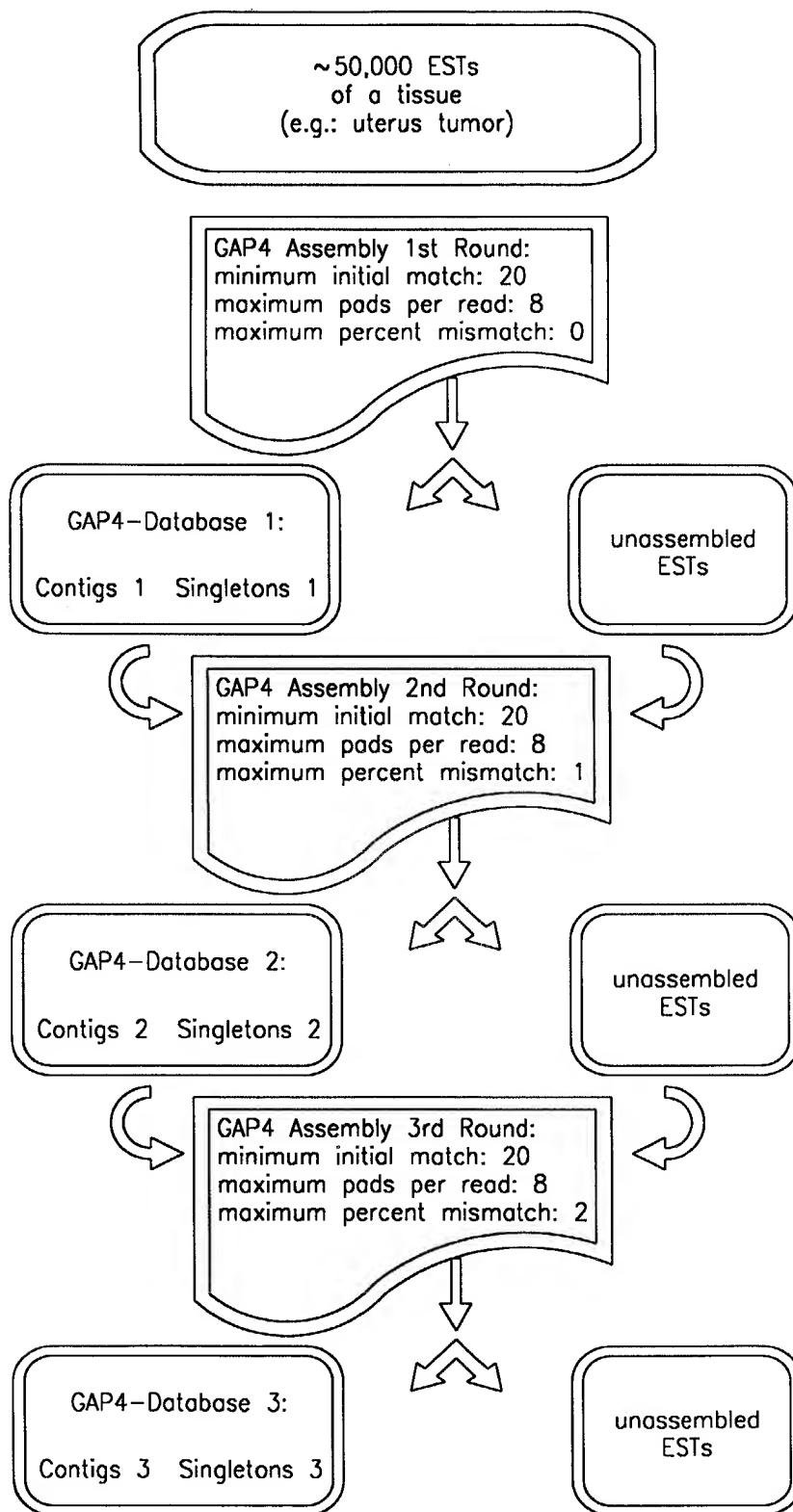


FIG. 2b-1

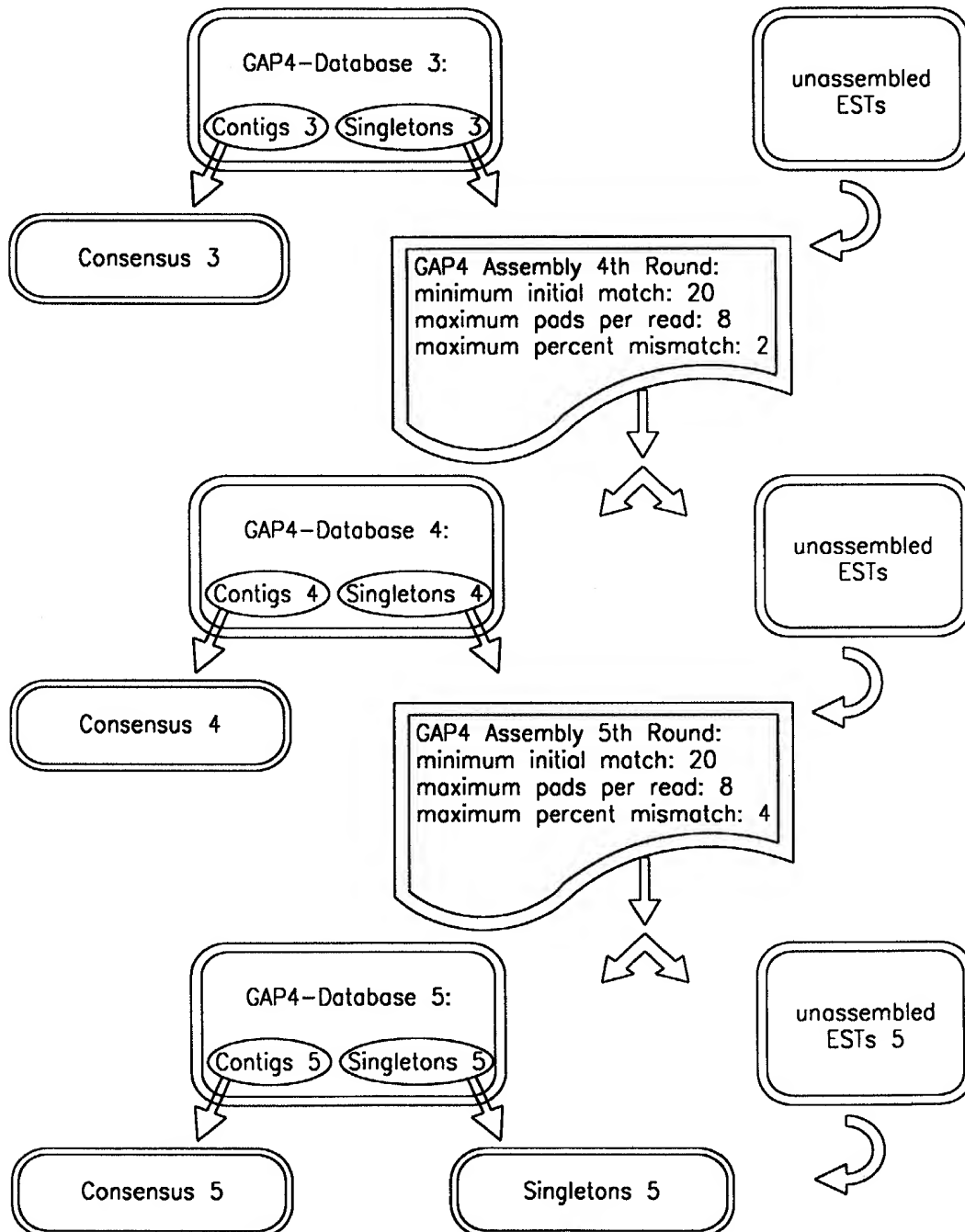


FIG. 2b-2

APPROVED	O. G. FIG.	
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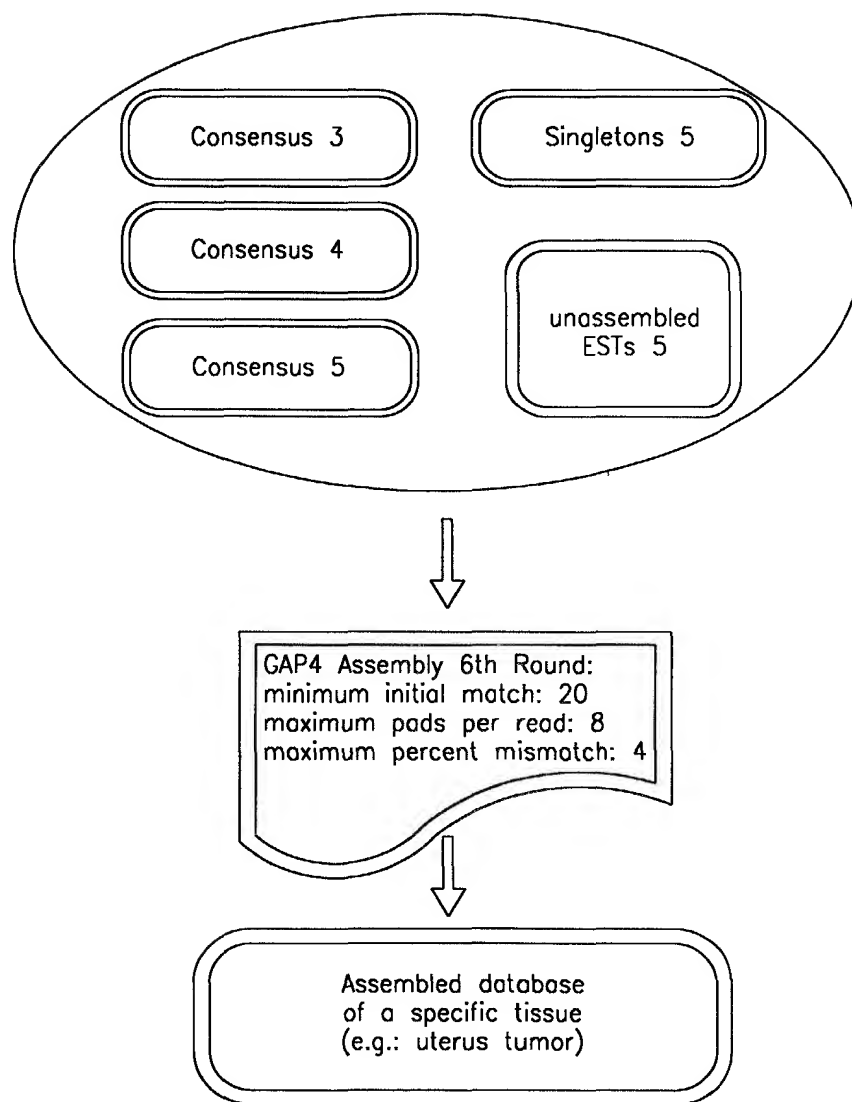


FIG. 2b-3

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
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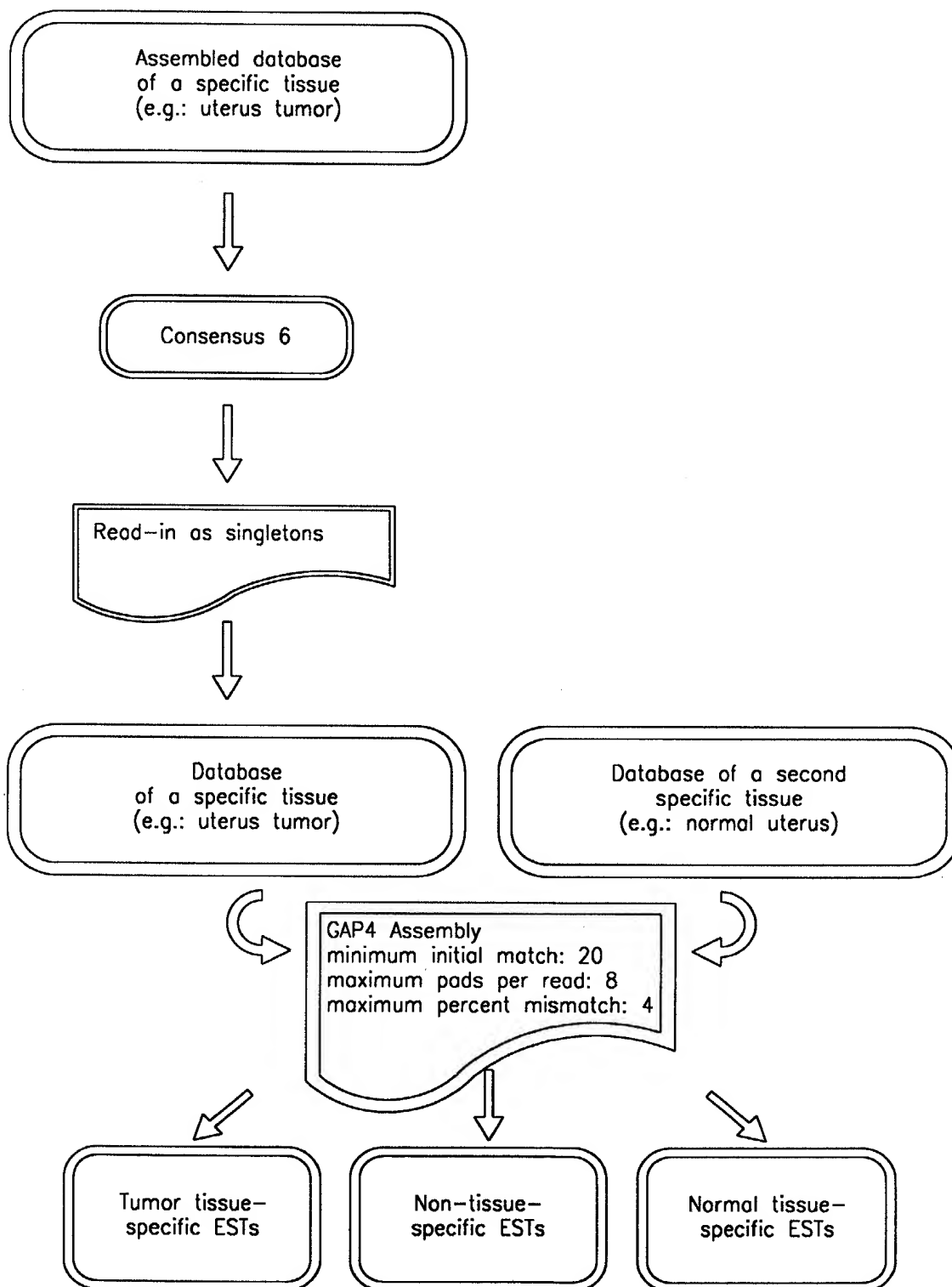


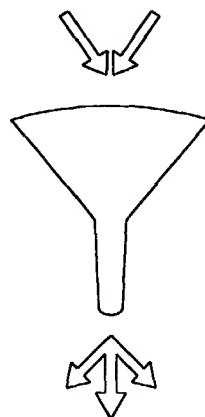
FIG. 2b-4

APPROVED	O. G. FIG.	
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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue



Assembly at 4% mismatch

Normal tissue
Specific genes

Cancer tissue
Specific genes

Genes expressed in both tissues

FIG. 3

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

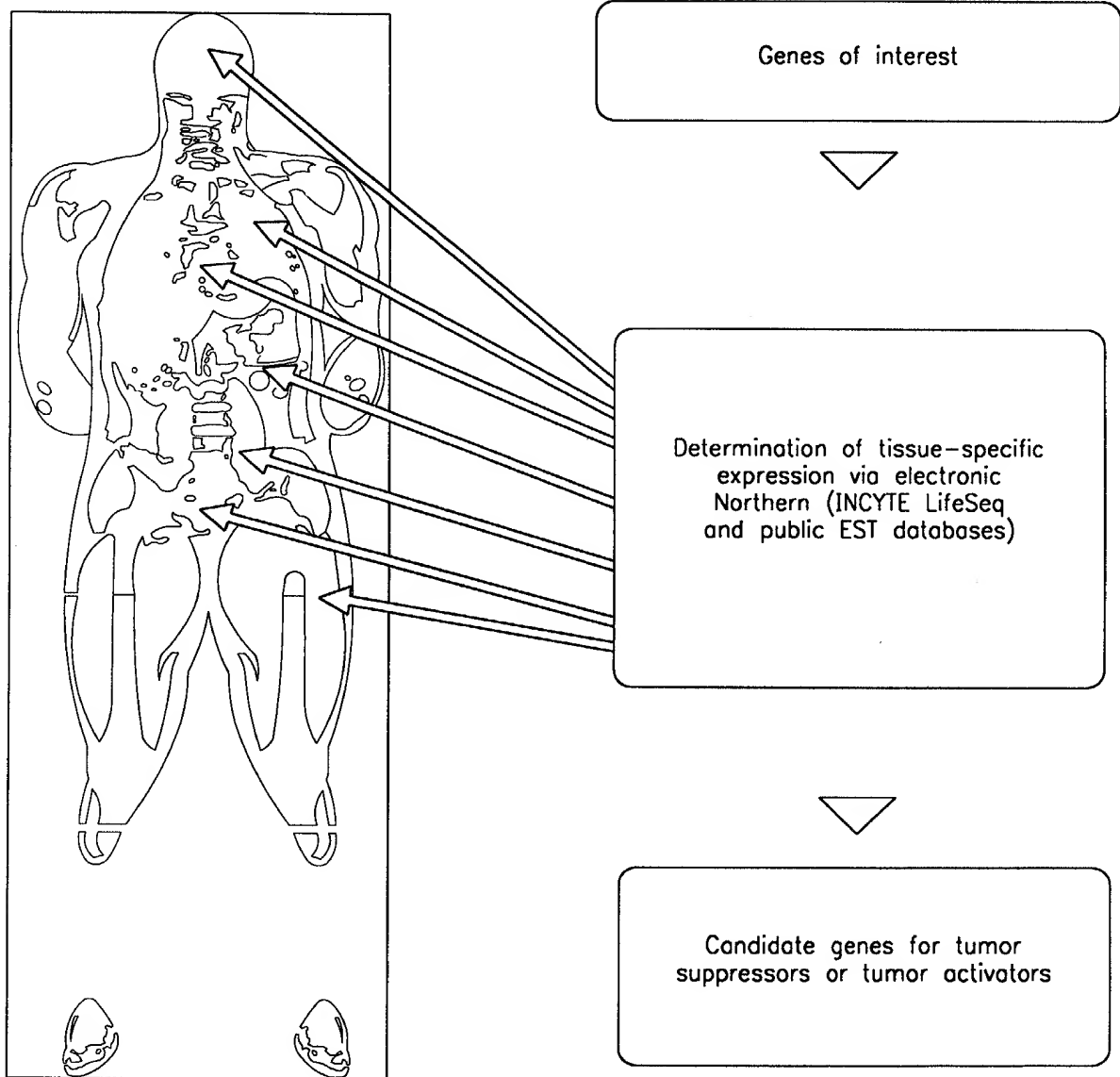


FIG. 4a

APPROVED	O. G. FIG.	
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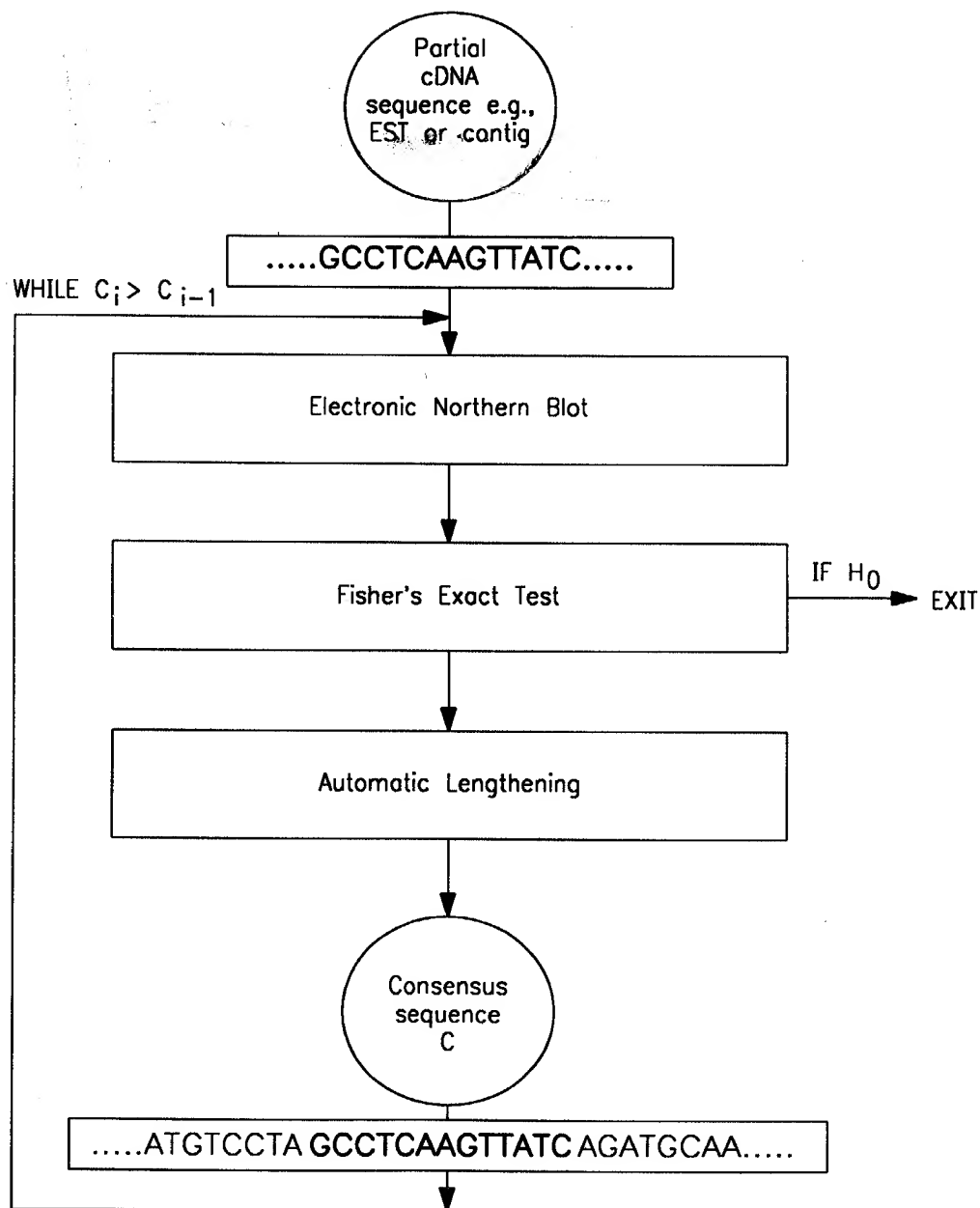


FIG. 4b

